In the Specification

On page 3 of the specification, following the paragraph that begins with "Both these approaches...", please add the following new section:

Brief Description of the Drawings

Figure 1. Shows a schematic overview of one embodiment of the present application.

Figure 2. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN1-001-A05.

Figure 3. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN1-001-B03.

Figure 4. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN1-001-F11.

Figure 5. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN15-001-A06.

Figure 6. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN14-001-H07.

Figure 7. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN16-001-B01.

Figure 8. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN15-C01.

Figure 9. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN16-001-C10.

Figure 10. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN15-H09.

Figure 11. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN17-001-C08.

Figure 12. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN17-001-E02.

Figure 13 Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvFN17-G07.

Figure 14. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvBITM7-001-A12.

Figure 15. Shows the results of the mass spectra analysis of peptides captured using the binding molecule scFvBITM12-001-E10.

On page 39, replace the first paragraph, with the following paragraph:

14 scFv's, designated scFvFN1-001-A05; scFvFN1-001-B03; scFvFN1-001-F11; scFvFN15-001-A06; scFvFN14-001-H07; scFvFN16-001-B01; scFvFN15-C01; scFvFN16-001-C10; scFvFN15-H09; scFvFN17-001-C08; scFvFN17-001-E02; scFvFN17-G07; scFvBITM7-001-A12; and scFvBITM12-001-E10, were selected based on their ability to capture different subgroups of peptides from trypsinated mouse liver proteins. The coupling reaction of scFv's to POROS-AL chromatography medium (Applied Biosystems, Foster City, USA) was performed in accordance with the manufacturer's instructions. The slurry was packed in gel loading tips (Invitrogen) to generate affinity columns with a bed length of approximately 2 cm.

On page 39, replace the second paragraph, with the following amended paragraph:

Mouse liver homogenate was alkylated and fragmented as above and diluted 2 times in PBS pH 7.4. The affinity columns were washed with 2.times.10 .mu.l 5% acetic acid and equilibrated with 2.times.10 .mu.l PBS pH 7.4. 10 .mu.l of the sample was loaded onto the column followed by washing with 2.times.10 .mu.l PBS pH 7.4. The column was eluted onto a Massprep MALDI target (Micromass, UK) with 7 .mu.l 5.% acetic acid. The eluate was allowed to dry and the target well was washed twice with 0.1% trifluoroacetic acid Finally 1 .mu.l of 0.5 mg/ml .alpha.-Cyano-4-hydroxy- -cinnamic acid in 75% acetonitrile/1% trifluoroacetic acid was added. The samples were analysed using a Micromass ~~M@ldi~~ Maldi Reflectron mass spectrometer